

SEQUENCE LISTING

<110> Broze, George J., Jr.

<120> Protein Z-Dependent Protease Inhibitor

<130> WU-3110/1

<140> 09/271,608

<141> 1999-03-17

<150> US 60/086,571

<151> 1998-05-19

<160> 16

<170> Word Perfect 5.0

<210> 1

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<221> Xaa=Unknown amino acid

<222> Xaa=Indeterminate residues 10 & 11; can be any amino acid

<223> /note="synthetic construct"

<400> 1

Leu Ala Pro Ser Pro Gln Ser Pro Glu Xaa Xaa Ala
1 5 10

<210> 2

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<221> Xaa=Unknown amino acid

<222> Xaa=Indeterminate residue 13; can be any amino acid

<223> /note="synthetic construct"

<400> 2

Arg Tyr Lys Gly Gly Ser Pro Xaa Ile Ser Gln Pro Xaa Leu
1 5 10

<210> 3

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> /note="synthetic construct"

<400> 3
acccagggtg gctttgcctt cat 23

<210> 4
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 4
gtacatcatg ggcaccttaa c 21

<210> 5
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 5
Asn Leu Glu Leu Gly Leu Thr Gln Ser Phe Ala Phe Ile His Lys
1 5 10 15

Asp Phe Asp Val

<210> 6
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<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 6
Met Ser Arg Ser Thr Gln Glu Leu Leu Gly Tyr His Cys Arg Leu
1 5 10 15

Gln Asp Lys Leu Gln Glu Gln Glu Gly Ser Leu Ala Ala Glu Gly
20 25 30

Arg His Ser Leu Ala Ser Ala Ala Asp His
35 40

<210> 7
<211> 2466
<212> DNA
<213> Artificial Sequence

<220>

<223> /note="synthetic construct"

<400> 7

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cagggatgtg tgctgtccca gggctgagaa gtggcagggtg agctgggtgat	200
tccttactgc ccaggttcgt tctaggaagg tgcgtcctca ccatgctgga	250
tggtgtccta gtccaggagc accccotgag ctcctggcct agactccaaa	300
gggttgggta gatgagcaaa gactttacaa agaccttagg cgatatatgt	350
ccaggagcac ccaggaatta ctgggctacc actgcagact gcaggacaag	400
ctccaagaac aggaagggaag tottgcagct gaagggaggc actccttggc	450
ctccgcagcc gat cac atg aag gtg gtg cca agt ctc ctg ctc	493
Met Lys Val Val Pro Ser Leu Leu Leu	
-20 -15	
tcc gtc ctc ctg gca cag gtg tgg ctg gta ccc ggc ttg gcc	535
Ser Val Leu Leu Ala Gln Val Trp Leu Val Pro Gly Leu Ala	
-10 -5 -1 1	
ccc agt cct cag tcg cca gag acc cca gcc cct cag aac cag	577
Pro Ser Pro Gln Ser Pro Glu Thr Pro Ala Pro Gln Asn Gln	
5 10 15	
acc agc agg gta gtg cag gct ccc aag gag gaa gag gaa gat	619
Thr Ser Arg Val Val Gln Ala Pro Lys Glu Glu Glu Glu Asp	
20 25 30	
gag cag gag gcc agc gag gag aag gcc agt gag gaa gag aaa	661
Glu Gln Glu Ala Ser Glu Glu Lys Ala Ser Glu Glu Glu Lys	
35 40	
gcc tgg ctg atg gcc agc agg cag cag ctt gcc aag gag act	703
Ala Trp Leu Met Ala Ser Arg Gln Gln Leu Ala Lys Glu Thr	
45 50 55	
tca aac ttc gga ttc agc ctg ctg cga aag atc tcc atg agg	745
Ser Asn Phe Gly Phe Ser Leu Leu Arg Lys Ile Ser Met Arg	
60 65 70	
cac gat ggc aac atg gtc ttc tct cca ttt ggc atg tcc ttg	787
His Asp Gly Asn Met Val Phe Ser Pro Phe Gly Met Ser Leu	
75 80 85	

gcc atg aca ggc ttg atg ctg ggg gcc aca ggg ccg act gaa	829
Ala Met Thr Gly Leu Met Leu Gly Ala Thr Gly Pro Thr Glu	
90 95 100	
acc cag atc aag aga ggg ctc cac ttg cag gcc ctg aag ccc	871
Thr Gln Ile Lys Arg Gly Leu His Leu Gln Ala Leu Lys Pro	
105 110	
acc aag ccc ggg ctc ctg cct tcc ctc ttt aag gga ctc aga	913
Thr Lys Pro Gly Leu Leu Pro Ser Leu Phe Lys Gly Leu Arg	
115 120 125	
gag acc ctc tcc cgc aac ctg gaa ctg ggc ctc aca cag ggg	955
Glu Thr Leu Ser Arg Asn Leu Glu Leu Gly Leu Thr Gln Gly	
130 135 140	
agt ttt gcc ttc atc cac aag gat ttt gat gtc aaa gag act	997
Ser Phe Ala Phe Ile His Lys Asp Phe Asp Val Lys Glu Thr	
145 150 155	
ttc ttc aat tta tcc aag agg tat ttt gat aca gag tgc gtg	1039
Phe Phe Asn Leu Ser Lys Arg Tyr Phe Asp Thr Gly Cys Val	
160 165 170	
cct atg aat ttt cgc aat gcc tca cag gcc aaa agg ctc atg	1081
Pro Met Asn Phe Arg Asn Ala Ser Gln Ala Lys Arg Leu Met	
175 180	
aat cat tac att aac aaa gag act cgg ggg aaa att ccc aaa	1123
Asn His Tyr Ile Asn Lys Glu Thr Arg Gly Lys Ile Pro Lys	
185 190 195	
ctg ttt gat gag att aat cct gaa acc aaa tta att ctt gtg	1165
Leu Phe Asp Glu Ile Asn Phe Glu Thr Lys Leu Ile Leu Val	
200 205 210	
gat tac atc ttg ttc aaa ggg aaa tgg ttg acc cca ttt gac	1207
Asp Tyr Ile Leu Phe Lys Gly Lys Trp Leu Thr Pro Phe Asp	
215 220 225	
cct gtc ttc acc gaa gtc gac act ttc cac ctg gac aag tac	1249
Pro Val Phe Thr Glu Val Asp Thr Phe His Leu Asp Lys Tyr	
230 235 240	
aag acc att aag gtg ccc atg atg tac ggt gca ggc aag ttt	1291
Lys Thr Ile Lys Val Pro Met Met Tyr Gly Ala Gly Lys Phe	
245 250	
gcc tcc acc ttt gac aag aat ttt cgt tgt cat gtc ctc aaa	1333
Ala Ser Thr Phe Asp Lys Asn Phe Arg Cys His Val Leu Lys	
255 260 265	

ctg ccc tac caa gga aat gcc acc atg ctg gtg gtc ctc atg Leu Pro Tyr Gln Gly Asn Ala Thr Met Leu Val Val Leu Met 270 275 280	1375
gag aaa atg ggt gac cac ctc gcc ctt gaa gac tac ctg acc Glu Lys Met Gly Asp His Leu Ala Leu Glu Asp Tyr Leu Thr 285 290 295	1417
aca gac ttg gtg gag aca tgg ctc aga aac atg aaa acc aga Thr Asp Leu Val Glu Thr Trp Leu Arg Asn Met Lys Thr Arg 300 305 310	1459
aac atg gaa gtt ttc ttt ccg aag ttc aag cta gat cag aag Asn Met Glu Val Phe Phe Pro Lys Phe Lys Leu Asp Gln Lys 315 320	1501
tat gag atg cat gag ctg ctt agg cag atg gga atc aga aga Tyr Glu Met His Glu Leu Leu Arg Gln Met Gly Ile Arg Arg 325 330 335	1543
atc ttc tca ccc ttt gct gac ctt agt gaa ctc tca gct act Ile Phe Ser Pro Phe Ala Asp Leu Ser Glu Leu Ser Ala Thr 340 345 350	1585
gga aga aat ctc caa gta tcc agg gtt tta caa aga aca gtg Gly Arg Asn Leu Gln Val Ser Arg Val Leu Gln Arg Thr Val 355 360 365	1627
att gaa gtt gat gaa agg ggc act gag gca gtg gca gga atc Ile Glu Val Asp Glu Arg Gly Thr Glu Ala Val Ala Gly Ile 370 375 380	1669
ttg tca gaa att act gct tat tcc atg cct cct gtc atc aaa Leu Ser Glu Ile Thr Ala Tyr Ser Met Pro Pro Val Ile Lys 385 390	1711
gtg gac cgg cca ttt cat ttc atg atc tat gaa gaa acc tct Val Asp Arg Pro Phe His Phe Met Ile Tyr Glu Glu Thr Ser 395 400 405	1753
gga atg ctt ctg ttt ctg ggc agg gtg gtg aat ccg act ctc Gly Met Leu Leu Phe Leu Gly Arg Val Val Asn Pro Thr Leu 410 415 420	1795
cta taa ttcaggacac gcataagcac ttgcgctgta gtagatgctg Leu 423	1841
aatotgaggt atcaaacaca cacaggatac cagcaatgga tggcagggga	1891
gagtgttcct tttgttctta actagttag ggtgttctca aataaataca	1941
gtagtcccca cttatctgag ggggatacat tcaaagaccc ccagcagatg	1991

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cctgaaacgg tggacagtgc tgaaccttat atatattttt tcctacacat      2041
acatacctat gataaagttt aatttataaa ttaggcacag taagagatta      2091
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aataccataa cagtcaaact gattatagag aaggctacta agtgactcat      2191
gggcgaggag catagacagt gtggagacat tgggcaaggg gagaattcac      2241
atcctgggtg ggacagagca ggacaatgca agattocatc ccaactactca      2291
gaatggcatg ctgcttaaga cttttagatt gtttatttct ggaatttttc      2341
atttaatggt tttggacat gggtgacat ggtaactga gactgcagaa      2391
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<210> 8

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> /note="synthetic construct"

<400> 8

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Met Lys Val Val Pro Ser Leu Leu Leu Ser Val Leu Leu Ala
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Val Val Trp Leu Val Pro Gly Leu Ala Pro Ser Pro Gln Ser
  -5                      -1  1                      5

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Pro Glu Thr Pro Ala Pro Gln Asn Gln Thr Ser Arg Val Val
  10                      15                      20

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Gln Ala Pro Lys Glu Glu Glu Glu Asp Glu Gln Glu Ala Ser
  25                      30                      35

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Glu Glu Lys Ala Ser Glu Glu Glu Lys Ala Trp Leu Met Ala
  40                      45

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Ser Arg Gln Gln Leu Ala Lys Glu Thr Ser Asn Phe Gly Phe
  50                      55                      60

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Ser Leu Leu Arg Lys Ile Ser Met Arg His Asp Gly Asn Met
  65                      70                      75

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Val Phe Ser Pro Phe Gly Met Ser Leu Ala Met Thr Gly Leu
  80                      85                      90

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Met Leu Gly Ala Thr Gly Pro Thr Glu Thr Gln Ile Lys Arg
95 100 105

Gly Leu His Leu Gln Ala Leu Lys Pro Thr Lys Pro Gly Leu
110 115

Leu Pro Ser Leu Phe Lys Gly Leu Arg Glu Thr Leu Ser Arg
120 125 130

Asn Leu Glu Leu Gly Leu Thr Gln Gly Ser Phe Ala Phe Ile
135 140 145

His Lys Asp Phe Asp Val Lys Glu Thr Phe Phe Asn Leu Ser
150 155 160

Lys Arg Tyr Phe Asp Thr Gly Cys Val Pro Met Asn Phe Arg
165 170 175

Asn Ala Ser Gln Ala Lys Arg Leu Met Asn His Tyr Ile Asn
180 185

Lys Glu Thr Arg Gly Lys Ile Pro Lys Leu Phe Asp Glu Ile
190 195 200

Asn Phe Glu Thr Lys Leu Ile Leu Val Asp Tyr Ile Leu Phe
205 210 215

Lys Gly Lys Trp Leu Thr Pro Phe Asp Pro Val Phe Thr Glu
220 225 230

Val Asp Thr Phe His Leu Asp Lys Tyr Lys Thr Ile Lys Val
235 240 245

Pro Met Met Tyr Gly Ala Gly Lys Phe Ala Ser Thr Phe Asp
250 255

Lys Asn Phe Arg Cys His Val Leu Lys Leu Pro Tyr Gln Gly
260 265 270

Asn Ala Thr Met Leu Val Val Leu Met Glu Lys Met Gly Asp
275 280 285

His Leu Ala Leu Glu Asp Tyr Leu Thr Thr Asp Leu Val Glu
290 295 300

Thr Trp Leu Arg Asn Met Lys Thr Arg Asn Met Glu Val Phe
305 310 315

Phe Pro Lys Phe Lys Leu Asp Gln Lys Tyr Glu Met His Glu
320 325

Leu Leu Arg Gln Met Gly Ile Arg Arg Ile Phe Ser Pro Phe
330 335 340

Ala Asp Leu Ser Glu Leu Ser Ala Thr Gly Arg Asn Leu Gln
345 350 355
Val Ser Arg Val Leu Gln Arg Thr Val Ile Glu Val Asp Glu
360 365 370
Arg Gly Thr Glu Ala Val Ala Gly Ile Leu Ser Glu Ile Thr
375 380 385
Ala Tyr Ser Met Pro Pro Val Ile Lys Val Asp Arg Pro Phe
390 395
His Phe Met Ile Tyr Glu Glu Thr Ser Gly Met Leu Leu Phe
400 405 410
Leu Gly Arg Val Val Asn Pro Thr Leu Leu
415 420

<210> 9
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 9

Glu Arg Gly Thr Glu Ala Val Ala Gly Ile Leu Ser Glu Ile Thr
1 5 10 15
Ala Tyr Ser Met Pro Pro Val Ile Lys Val Asp Arg Pro Phe His
20 25 30
Phe Met Ile Tyr Glu Glu Thr Ser Gly Met Leu Leu Phe Leu Gly
35 40 45
Arg Val Val Asn Pro Thr Leu Leu
50

<210> 10
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 10

Glu Arg Gly Thr Glu Val Val Ser Gly Thr Val Ser Glu Ile Thr
1 5 10 15

Ala Tyr Cys Met Pro Pro Val Ile Lys Val Asp Arg Pro Phe His
20 25 30
Phe Ile Ile Tyr Glu Glu Met Ser Arg Met Leu Leu Phe Leu Gly
35 40 45
Arg Val Val Asn Pro Thr Val Leu
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<210> 11
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 11
Glu Lys Gly Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile
1 5 10 15
Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val
20 25 30
Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly
35 40 45
Lys Val Val Asn Pro Thr Gln Lys
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<210> 12
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 12
Glu Lys Gly Thr Glu Ala Thr Gly Ala Pro His Leu Glu Glu Lys
1 5 10 15
Ala Trp Ser Lys Tyr Gln Thr Val Met Phe Asn Arg Pro Phe Leu
20 25 30
Val Ile Ile Lys Glu Tyr Ile Thr Asn Phe Pro Leu Phe Ile Gly
35 40 45
Lys Val Val Asn Pro Thr Gln Lys
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<210> 13
<211> 56
<212> PRT

<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 13
Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr Ala Val Val Ile Ala
1 5 10 15
Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe Lys Ala Asn Arg
20 25 30
Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn Thr Ile Ile
35 40 45
Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
50 55

<210> 14
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 14
Glu Glu Gly Thr Gln Ala Thr Thr Val Thr Thr Val Gly Phe Met
1 5 10 15
Pro Leu Ser Thr Gln Val Arg Phe Thr Val Asp Arg Pro Phe Leu
20 25 30
Phe Leu Ile Tyr Glu His Arg Thr Ser Cys Leu Leu Phe Met Gly
35 40 45
Arg Val Ala Asn Pro Ser Arg Ser
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<210> 15
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> /note="synthetic construct"

<400> 15

Glu Asp Gly Thr Lys Ala Ser Ala Ala Thr Thr Ala Ile Leu Ile
1 5 10 15

Ala Arg Ser Ser Pro Pro Trp Phe Ile Val Asp Arg Pro Phe Leu
20 25 30

Phe Phe Ile Arg His Asn Pro Thr Gly Ala Val Leu Phe Met Gly
35 40 45

Gln Ile Asn Lys Pro
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<210> 16

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> /note="synthetic construct"

<400> 16

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